

SEQUENCE LISTING

Tab 50 X (1) GENERAL INFORMATION:

- (i) APPLICANT: MAERTENS, GEERT
STUYVER, LIEVEN
- (ii) TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
- (iii) NUMBER OF SEQUENCES: 207
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: ARNOLD, WHITE & DURKEE
(B) STREET: P.O. BOX 4433
(C) CITY: HOUSTON
(D) STATE: TEXAS
(E) COUNTRY: USA
(F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word 6.0 / ASCII text output
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/836,075
(B) FILING DATE: 21 Apr 1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP95/04155
(B) FILING DATE: 23 Oct 1995
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP 94870166.9
(B) FILING DATE: 21 Oct 1994
- (ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP 95870076.7
(B) FILING DATE: 28 Jun 1995
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: KAMMERER, PATRICIA A.
(B) REGISTRATION NUMBER: 29,775
(C) REFERENCE/DOCKET NUMBER: INNS:004

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid

65

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTCAK 60
GGSGTNNNNN NNCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG 120
GGCCCCAGGN NGGGTGTGCG CGCGACTAGG AAGACTTCCG AGCGGTCACA ACCTCGTGGC 180
AGGCGACAGC CTATCCCCAA GGCTCGYCGG YCCGAGGGCA GGTCTGGGC TCAGCCCGGG 240
TATCCTTGGC CCCTCTATGG CAATGAGGGC TCGGGGTGGG CGGGNTGGCT CCTGTCCCCC 300
CGCGGCTCTC GGCCCAATTG GGGCCCC 327

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15
Arg Arg Pro Xaa Xaa Xaa Xaa Xaa Pro Gly Gly Gly Gln Ile Val Gly
20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Xaa Gly Val Arg Ala
35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60
Ile Pro Lys Ala Xaa Arg Xaa Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro
100 105

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GACGGCGTGA ACTATGCAAC AGGGAAGTTG CCCGGTTGCT CTTTCTCTAT CTTCTCTTG 60
GCTTTGCTGT CCTGCTTGAC GGTTCACACK ACCGCTCACG AGGTGCGCAA CGCATCCGGG 120
GTGTATCATG TCACCAACGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GGACGGTATG 180
ATCATGCACT ACCCAGGGTG CGTGCCCTGC GTTCGGGAGG ATAACCATCT CCGCTGCTGG 240
ATGGCGCTCA CCCCCACGCT TGCGGTCAAA AAYGCTAGTG TCCCCACTRC GGCAATCCGA 300
CGTCACGTCG ACTTGCTTGT TGGGGGNNCC ACGTTCTGTT CCGCTATGTA CGTGGGGRGAC 360
CTTTGCGGGT CTGTCTTCCT CGCTGGCCAG CTATTCACCT TTTCACCCCG CATGCACCAT 420
ACAACGCAGG AGTGCAACTG CTCAATC 447

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser

67

1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Xaa Thr Ala
20 25 30

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp Cys
35 40 45

Ser Asn Ser Ser Ile Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
50 55 60

Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn His Leu Arg Cys Trp
65 70 75 80

Met Ala Leu Thr Pro Thr Leu Ala Val Lys Xaa Ala Ser Val Pro Thr
85 90 95

Xaa Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Xaa Xaa Thr Phe
100 105 110

Cys Ser Ala Met Tyr Val Xaa Asp Leu Cys Gly Ser Val Phe Leu Ala
115 120 125

Gly Gln Leu Phe Thr Phe Ser Pro Arg Met His His Thr Thr Gln Glu
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCACAG 60

GACGTCAAGN TCCCGGGTGG TGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG 120

GGCCCCAGGT TGGGTGTGCG CGCGACCAGG AAGACTTCCG AGCGGTCGCA GCCTCGTGAC 180

AGGCGACAGC CTATTCCTAA GGCTCGCCAG TCCGATGGCA GNNCCTGGGC TCAGCCAGGG 240

CATCCCTGGC CCCTCTATGG CAATGAGGGC TCGGATGGG CGGGATGGCT CCTGTCCCCC 300
CGCGGCTCTC GGCCAGTTG GGGCCCC 327

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Xaa Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Asp Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Gln Ser Asp Gly Xaa Xaa Trp Ala Gln Pro Gly
 65 70 75 80
 His Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro
 100 105

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GACGGCGTGA ACTATGCAAC AGGGAATTTG CCTGGTTGCT CTTTCTCTAT CTTCCTCTTA 60
GCTTTTCTGT CCTGCTTGAC GGTTCCTCACT ACCGCTCATG AGGTGCGCAA CGCATCCGGG 120
GTATATCATC TCACCAATGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GAGTGGTATG 180
ATCTTGCACG CCCCAGGGTG TGTGCCCTGC GTTCGGGAGA ACAACTCTTC TCGTTGCTGG 240
ATGCCRCTCA CCCCCACGCT TCGGGTCAAA GACGCTAATG TCCCTACTGC GGCAATCCGA 300
CGCCATGTCG ACTTGCTGGT TGGGACAGCC GCGTTTCGTT CCGCTATGTA CGTGGGGGAC 360
CTCTGCGGAT CCGTCTTCCT TGTGCGCCAG CTATTCACCT TTTCACCCCG CTTGTACCAT 420
ACAACACAGG AGTGCAACTG CTCAATC 447

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Phe Leu Ser Cys Leu Thr Val Pro Thr Thr Ala
20 25 30
His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu Thr Asn Asp Cys
35 40 45
Ser Asn Ser Ser Ile Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp
65 70 75 80
Met Xaa Leu Thr Pro Thr Leu Ala Val Lys Asp Ala Asn Val Pro Thr
85 90 95
Ala Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Thr Ala Ala Phe
100 105 110
Arg Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val

70

115	120	125
Gly Gln Leu Phe Thr Phe Ser Pro Arg Leu Tyr His Thr Thr Gln Glu		
130	135	140
Cys Asn Cys Ser Ile		
145		

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACCAACCG CCGCCCACAG	60
GACGTCAAGT TCCCGGGCGG TGGCCAGATC GTTGGTGGAG TCTACGTGCT ACCGCGCAGG	120
GGCCCTAGAT TGGGTGTGCG CGCAGCGCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG	180
AGGCGCCAAC CTATTCCCAA GGAGCGCCGA CCCGAGGGCA GGT	223

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20	30
Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	

71

35

40

45

Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg
65 70

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGCA ACACCAACCG CCGCCCACAG 60
GACGTTAAAT TCCCGGGTGG GGGGCAGATC GTGGGTGGAG TTTACTTGTT GCCGCGCAGG 120
GGCCCCAGGT TGGGTGTGCG CGCGACGAGG AAGACTTCCG AGCGGTCGCA ACCTCGCGGA 180
AGGCGACAGC CTATCCCCAA GGCTCGCCGA CCCGAGGGCA GGTCTTGGGC TCAGCCTGGG 240
TACCCATGGC CCCTCTATGC TAACGAGGGC TGCGGATGGG CGGGATGGCT CCTGTCCCCCT 300
CGCGGCTCCC GTCCTAGCTG GGGCCCCAAT GACCCCCGAC GTAGATCACG CAATTTGGGT 360
AAGGTCATCG ATACCCTAAC GTGTGGCTTC GCCGATCTCA TGGGGTACAT TCCGCTCGTC 420
GGCGCCCCCC TAGGGGGCGC TTCCAGAACC CTGNCACATG GTGTCCGGGT CCTGGNAGGC 480
GGCGTGATNN NNNNNNNNNN NAACCTTCN GGTGCTCTT TNNCTATCTT CCTCTTGGCN 540
TTACTCTCTT GCCTCACAGT CCCCACCTCT GCCTATGAGG TGCACAGCAC AACCGATGGC 600
TACCATGTCA CTAATGACTG TTCCAACGGC AGCATCGTAT ATGAGGCAAA GGACATCATC 660
CTTCACACGC CTGGGTGNGT GCCCTGCATA CGGGAAGGCA ATATCTCCCG TTGCTGGGTA 720
CCGCTCACCC CCACGCTCGC AGCGCGGATC GCGAACGCTC CCATCGATGA GGTGCGGCGT 780
CACGTCGACC TCCTCGTGGG GGCAGCCGTG TTCTGCTCAG CCATGTACAT TGGGGACCTT 840

72

TGTGGGGGCG TCTTCCTCGT TGGGCAATTG TTCACCTTCA CGTCCCGGCG GCATTGGACG 900
 GTGCAGGACT GTAATTGTTC CATTTACTCT GGCCACATAA CGGGCCACCG NNNNNNN 957

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
 130 135 140
 Gly Gly Ala Ser Arg Thr Leu Xaa His Gly Val Arg Val Leu Xaa Gly
 145 150 155 160
 Gly Val Xaa Xaa Xaa Xaa Xaa Asn Leu Xaa Gly Cys Ser Xaa Xaa Ile
 165 170 175
 Phe Leu Leu Xaa Leu Leu Ser Cys Leu Thr Val Pro Thr Ser Ala Tyr
 180 185 190
 Glu Val His Ser Thr Thr Asp Gly Tyr His Val Thr Asn Asp Cys Ser

195 200 205
 Asn Gly Ser Ile Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr Pro
 210 215 220
 Gly Xaa Val Pro Cys Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val
 225 230 235 240
 Pro Leu Thr Pro Thr Leu Ala Ala Arg Ile Ala Asn Ala Pro Ile Asp
 245 250 255
 Glu Val Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Val Phe Cys
 260 265 270
 Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu Val Gly
 275 280 285
 Gln Leu Phe Thr Phe Thr Ser Arg Arg His Trp Thr Val Gln Asp Cys
 290 295 300
 Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly His Xaa Xaa Xaa
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ATACCAACCG CCGCCCACAG	60
GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGAT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCACGTGGA	180
AGGCGCCAGC CCATCCCTAA AGATCGGNGN GCCACTGGCA GGTCCCTGGGG ACGTCCAGGA	240
TATCCCTGGC CCCTGTATGG GAACGAGGGG CTCGGCTGGG CAGGATGGCT CCTGTCCCCC	300
CGAGGCTCTC	310

(2) INFORMATION FOR SEQ ID NO: 14:

74

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Asp Arg Xaa Ala Thr Gly Arg Ser Trp Gly Arg Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly
 100 105

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACGTGCGGNT NTGCCGACCT CATGGGGTAC ATNCCCGTTG TCGGCGCCCC GGTGGGCGGG 60
 GTNGCCAGGG CCCTCGCGNA TGGCGTGCGG GTCCTGGAGG ACGGGATAAA TTATGNAACA 120

75

GGGAACCTCC CTGGTTGCTC CTTTTCTATC TTCTNGTTGG CTCTTCTGTC TTGTGTCACC 180
 GTGCCTGTCT CTGNCGTTGA GGTCAAAAAT ACCAGTCAGG CCTATATGGC AACCAACGAC 240
 TGCTCCAACA ACAGCATCGT ATGGCAATTG GNGGACGCGG TGCTTCATGT TCCTGGATGT 300
 GTCCCCTGCG AGAATAGCTC CGGTCGGTTC CACTGTTGGA TCCCGATCTC GCCCAACATA 360
 GCCGTGAGCA AACCTGGTGC TCTACCAAG GGA CTGCGGG CACGCATTGA TGCCGTCGTG 420
 ATGTCCGCCA CCCTCTGCTC TGCCCTGTAC GTGGGAGATG TGTGCGGCGC AGTGATGATA 480
 GCTGCACAGG CTTTCATCGT GGCACCGAAG CGCCATTACT TCGTCCAGGA ATGCAATTGC 540
 TCCATATAACC CAGGCCACAT TACAGGTCAT CGCATGGCG 579

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Thr	Cys	Xaa	Xaa	Ala	Asp	Leu	Met	Gly	Tyr	Xaa	Pro	Val	Val	Gly	Ala
1				5				10						15	
Pro	Val	Gly	Gly	Xaa	Ala	Arg	Ala	Leu	Ala	Xaa	Gly	Val	Arg	Val	Leu
		20						25					30		
Glu	Asp	Gly	Ile	Asn	Tyr	Xaa	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
		35						40					45		
Ser	Ile	Phe	Xaa	Leu	Ala	Leu	Leu	Ser	Cys	Val	Thr	Val	Pro	Val	Ser
		50				55					60				
Xaa	Val	Glu	Val	Lys	Asn	Thr	Ser	Gln	Ala	Tyr	Met	Ala	Thr	Asn	Asp
65				70						75				80	
Cys	Ser	Asn	Asn	Ser	Ile	Val	Trp	Gln	Leu	Xaa	Asp	Ala	Val	Leu	His
			85						90					95	
Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Ser	Ser	Gly	Arg	Phe	His	Cys
			100					105					110		
Trp	Ile	Pro	Ile	Ser	Pro	Asn	Ile	Ala	Val	Ser	Lys	Pro	Gly	Ala	Leu
			115					120					125		

76

Thr Lys Gly Leu Arg Ala Arg Ile Asp Ala Val Val Met Ser Ala Thr
 130 135 140
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys Gly Ala Val Met Ile
 145 150 155 160
 Ala Ala Gln Ala Phe Ile Val Ala Pro Lys Arg His Tyr Phe Val Gln
 165 170 175
 Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
 180 185 190
 Ala

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACTAAAAGAA AACTAACC GTCGCCACAG 60
 GACGTTAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG 120
 GGCCCCAGGT TGGGTGTGCG CGCGCCAAGG AAGACTTCTG AACGGTCCCA GCCACGTGGA 180
 AGGCGCCAGC CCATCCCCAA AGATCGGCGC GCCACTGGCA AGTCCTGGGG ACGTCCAGGA 240
 TACCCTTGGC CCCTGTACGG GAACGAGGGC CTCGGCTGGG CAGGGTGGCT CCTGTCCCCC 300
 CGGGGCTCTC GCCCCTCGTG GGGCCCCAAAC GACCCCCGGC ACAGGTCACG CAACTTGGGT 360
 AAGGTCATCG ATACCCTCAC GTGTGGCTTT GSCGACCTCA TGGGGTACAT ACCTGTCGTC 420
 GGCGCCCCCTG TGGGCGGCGT TGCCAGAGCC CTCGCGCATG GCGTGCGGGT CCTGGAGGAC 480
 GGGATAAATT ATGCAACAGG GAACTTGCCC GGTGCTCCT TTTCTATCTT CTTGCTGGCT 540
 CTCTTGCTCT GTATCACCGT GCCCCTGTCT GCCATACAGG TTAAGAACAA CAGCCACTTC 600
 TACATGGCGA CTAATGACTG TGCCAATGAC AGCATCGTCT GGCAGCTCAG GGACGCGGTG 660

77

CTCCATGTTC CTGGATGTGT CCCCTGTGAG AGGTCAGGTA ATAGGACCTT CTGTTGGACA 720
 GCGGTCTCGC CCAACGTGGC TGTGAGCCGA CCTGGTGCTC TCACTAGAGG TCTGCGGGCT 780
 CACATTGATA CCATCGTGAT GTCCGCCACC CTCTGCTCTG CCCTATACAT AGGGGACCTA 840
 TGCGGCGCTG TGATGATAGC AGCGCAAGTT GCCGTCGTCT CACCGCAATA CCATACTTTT 900
 GTCCAGGAAT GCAACTGCTC CATATACCCA GGCCATATCA CAGGACATCG AATGGNN 957

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Pro Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Asp Arg Arg Ala Thr Gly Lys Ser Trp Gly Arg Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Xaa Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

78

Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala Ile
 180 185 190
 Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala Thr Asn Asp Cys Ala
 195 200 205
 Asn Asp Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
 210 215 220
 Gly Cys Val Pro Cys Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr
 225 230 235 240
 Ala Val Ser Pro Asn Val Ala Val Ser Arg Pro Gly Ala Leu Thr Arg
 245 250 255
 Gly Leu Arg Ala His Ile Asp Thr Ile Val Met Ser Ala Thr Leu Cys
 260 265 270
 Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Ile Ala Ala
 275 280 285
 Gln Val Ala Val Val Ser Pro Gln Tyr His Thr Phe Val Gln Glu Cys
 290 295 300
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Xaa
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GACGGGGTAA ATTATGCAAC AGGGAATCTG CCTGGTTGCT CTTTCTCTAT CTTCTTGTTG	60
GCTCTTCTGT CTTGTGTCAC CGTGCCTGTC TCTGCCGTGC AGGTTAAGAA CACCAGTACC	120
ATGTACATGG CAACCAATGA CTGTTCCAAC AACAGCATCA TCTGGCAAAT GCAGGGCGCG	180

GTGCTTCATG TTCCTGGATG TGTCCCGTGT GAGTTGCAGG GCAATAAGTC CCGGTGCTGG 240
 ATACCGGTCA CTCCCAACGT GGCTGTGAAC CAGCCCGGCG CCCTCACTAG GGGCTTGCGG 300
 ACGCACATTG ACACCATCGT GATGGTCGCT ACGCTCTGTT CTGCACTCTA CATCGGGGAC 360
 GTGTGTGGCG CGGTGATGAT AGCTGCTCAG GTTGTCAATTG TCTCGCCGCA ACATCACAAC 420
 TTTTCCCAGG ATTGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
 1 5 10 15
 Ile Phe Leu Leu Ala Leu Leu Ser Cys Val Thr Val Pro Val Ser Ala
 20 25 30
 Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala Thr Asn Asp Cys
 35 40 45
 Ser Asn Asn Ser Ile Ile Trp Gln Met Gln Gly Ala Val Leu His Val
 50 55 60
 Pro Gly Cys Val Pro Cys Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp
 65 70 75 80
 Ile Pro Val Thr Pro Asn Val Ala Val Asn Gln Pro Gly Ala Leu Thr
 85 90 95
 Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Met Val Ala Thr Leu
 100 105 110
 Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Val Met Ile Ala
 115 120 125
 Ala Gln Val Val Ile Val Ser Pro Gln His His Asn Phe Ser Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 21:

80

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA AACTAACC GCGCCACAG 60
GACGTTAAGT TCCCGGGCGG TGGCCAGATC GTTGGCGGAG TATACTTGTT GCCGCGCAGG 120
GGCCCCCGGT TGGGTGTGCG CGCGACGAGG AAAACTTCCG AACGGTCCCA GCCACGTGGG 180
AGGCGCCAGC CCATCCCTAA AGATCGGCGC TCCACTGGCA AATCCTGGGG ACGTCCAGGA 240
TACCCTTGGC CCCTGTATGG GAACGAGGGC CTTGGTTGGG CAGGATGGCT CTTGTCCCCT 300
CGAGGCTCTC 310

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Arg Ser Leu Ala
20 25 30
Glu Tyr Thr Cys Ala Arg Arg Gly Lys Leu Arg Arg Ser Ser Met Gly
35 40 45

(2) INFORMATION FOR SEQ ID NO: 23:

81

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GACGGGATAA ACTACGCAAC AGGGAATCTG CCCGGTTGCT CCTTTTCTAT CTTCTTGCTG 60
GCCTTGCTAT CCTGTCTCAC TGTGCCGGCG TCCGCTGTGC AGGTCAAGAA CACCAGCCAC 120
TCTTATATGG TGACCAATGA TTGCTCAAAC AGCAGCATTG TCTGGCAGCT TAAGGATGCT 180
GTGCTTCACG TCCCTGGATG TGTTCCATGT GAGAGGCACC AAAATCAGTC TCGCTGCTGG 240
ATACCTGTGA CACCCAATGT GGCCGTGAGC CAACCTGGCG CGCTCACCAG GGGTTTGCGG 300
ACGCACATTG ACACCATCGT TGCGTCTGCT ACCGTCTGCT CAGCTTTGTA TGTGGGCGAC 360
TTCTGCGGCG CAGTGATGTT GGTCTCTCAA TTTTTCATGA TCTCCCCTCA GCACCACATC 420
TTCGTCCAGG ATTGCAACTG CTCGATA 447

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Val Gln Val Lys Asn Thr Ser His Ser Tyr Met Val Thr Asn Asp Cys
35 40 45

82

Ser Asn Ser Ser Ile Val Trp Gln Leu Lys Asp Ala Val Leu His Val
 50 55 60
 Pro Gly Cys Val Pro Cys Glu Arg His Gln Asn Gln Ser Arg Cys Trp
 65 70 75 80
 Ile Pro Val Thr Pro Asn Val Ala Val Ser Gln Pro Gly Ala Leu Thr
 85 90 95
 Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Ala Ser Ala Thr Val
 100 105 110
 Cys Ser Ala Leu Tyr Val Gly Asp Phe Cys Gly Ala Val Met Leu Val
 115 120 125
 Ser Gln Phe Phe Met Ile Ser Pro Gln His His Ile Phe Val Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACGGGATAA ACTATGCAAC AGGGAACCTG CCTGGTTGCT CCTTTTCTAT CTTCTTACTG	60
GCCCTGCTTT CTTGCATCAC CGTGCCGGTC TCTGCCGTGC AAGTTGCGAA CCGCAGTGGT	120
TCTTACATGG TGACCAATGA TTGCTCGAAC AGCAGCATCG TTTGGCAGCT CGAGGAGGCC	180
GTCCTTCACG TCCCTGGATG TGTTCCCTGT GAGTGGAAGG ACAACACCTC CCGCTGCTGG	240
ATACCGGTCA CCCCTAACAT CGCTGTGAGC CAACCTGGCG CGCTTACCAA GGGCCTGCGG	300
ACACATATTG ACATCATTGT CGCGTCCGCC ACGTTCTGCT CTGCCTTGTA TGTGGG	356

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:

83

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala
20 25 30

Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val Thr Asn Asp Cys
35 40 45

Ser Asn Ser Ser Ile Val Trp Gln Leu Glu Glu Ala Val Leu His Val
50 55 60

Pro Gly Cys Val Pro Cys Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp
65 70 75 80

Ile Pro Val Thr Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Xaa Thr
85 90 95

Lys Gly Leu Arg Thr His Ile Asp Ile Ile Val Ala Ser Ala Thr Phe
100 105 110

Cys Ser Ala Leu Tyr Val
115

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCCATG

60

84

GACGTTAAGT TCCCGGGTGG TGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG 120
 GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG 180
 AGACGCCAAC CTATCCCCAA GGCGCGTCGA TCCGAGGGAA GGTCCTGGGC ACAGCCAGGA 240
 TATCCATGGC CTCTTTACGG TAATGAGGGT TGCGGGTGGG CANNATGGCT CTTGTCCCCC 300
 CGCGGTTCTC 310

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg
 115

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

85

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GACGGGATCA ATTTTGCAAC AGGGAACCTC CCCGGTTGCT CCTTTTCTAT CTTCCTCTTG 60
GCACTCCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCATCA ACTATCGCAA TGTCTCGGGC 120
ATTTACTATG TCACCAATGA TTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC 180
ATCTTGCAAC TCCCAGGTTG CGTGCCCTGC GTGAGAGAGG GGAATCAGTC ACGTTGCTGG 240
GTAGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG 300
AGTCATGTGG ACTTGATGGT GGGGGCCGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAT 360
TTRTGTGGYG GCTTGTTCTT AGTCGGTCAG ATGTTCTCTT TCCGACCAAG GCGCCACTGG 420
ACTACTCAAG ATTGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val Thr Asn Asp Cys
35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser Arg Cys Trp
65 70 75 80

86

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Xaa Cys Xaa Gly Leu Phe Leu Val
115 120 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GACGGGATCA ATTATGCAAC AGGGAACCTT CCCGGTTGCT CTTTTTCTAT CTCCTCTTG 60

GCACTCCTCT CGTGCCTGAC TGTTCCCGCT TCGGCCATTA ACTACGCAA CACCTCGGGC 120

ATCTACCACG TCACCAATGA CTGCCCCGAAC TCGAGCATAG TTTATGAGGC CGACCACCAC 180

ATCTTGCACC TTCCAGGTTG CGTGCCCTGC GTGAGAACTG GGAATCAGTC ACGTTGCTGG 240

GTGGCCCTTA CTCCTACCGT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCTCTGCGG 300

AGTCATGTGG ATCTGATGGT GGGGGCTGCC ACTGTTTGCT CAGCCCTTTA CATCGGGGAT 360

TTGTGTGGCG GCTTGTTCTT GGTGAGTCAG ATGTTTCTT TCCGACCACG ACGCCACTGG 420

ACTGCCCAGG ATTGCAATTG TTCTATC 447

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids

87

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val Thr Asn Asp Cys
35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys Trp
65 70 75 80
Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95
Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110
Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
115 120 125
Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Ala Gln Asp
130 135 140
Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GACGGGATTA ATTATGCAAC AGGGAATCTT CCCGGTTGCT CCTTTTCTAT CTTCTCTTG 60
GCACTTCTCT CGTGCCTGAC TGTCCCGCT TCGGCCATTA ACTACCACAA CACCTCGGGC 120
ATCTATCATA TCACCAACGA CTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC 180
ATCTTGCATC TCCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAATCAGTC GAGTTGCTGG 240
GTGGCCCTTA CCCCTACCAT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCCTTGCGG 300
AGTCATGTGG ATCTGATGGT GGGGGCGGCC ACTGTCTGTT CAGCCCTTTA CATCGGGGAT 360
TTGTGTGGCG GTGCGTTCTT GGTGGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG 420
ACCACCCAAG ATTGCAACTG CTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp Cys
35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Ser Cys Trp
65 70 75 80
Val Ala Leu Thr Pro Thr Ile Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95
Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110
Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ala Phe Leu Val

89

115

120

125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp
 130 135 140

Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GACGGGATCA ATTATGCAAC AGGGAATATT CCCGGTTGCT CYTTTTCTAT CTTCCCTTYTG 60
 GCACTTCTCT CGTGTCTGAC TGTCCCCGCT TCGGCCACTA ACTATCGCAA CGTCTCGGGC 120
 ATCTACCATG TCACCAATGA CTGCCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC 180
 ATCTTAGCAC TTCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAACCAGTC ACGCTGCTGG 240
 GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACACCGCGG CGCCGCTTGA GTCCCTGCGG 300
 AGTCATGTGG ATCTGATGGT GGGAGCTGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAY 360
 TTGTGTGGCG GCTTGTCTTT GGTGGTTCAG ATGTTCTCTT TYCAGCCTCG GCGCCACTGG 420
 ACTACCCAGG ATTGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

90

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Ile Pro Gly Cys Xaa Phe Ser
 1 5 10 15
 Ile Phe Leu Xaa Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
 20 25 30
 Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 35 40 45
 Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu Ala Leu
 50 55 60
 Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys Trp
 65 70 75 80
 Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Thr Ala Ala Pro Leu
 85 90 95
 Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
 100 105 110
 Cys Ser Ala Leu Tyr Ile Gly Xaa Leu Cys Gly Gly Leu Phe Leu Val
 115 120 125
 Gly Gln Met Phe Ser Xaa Gln Pro Arg Arg His Trp Thr Thr Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GACGGGATTA ATTATGCAAC AGGGAAYCTC CCCGGTTGCT CTTTTTCTAT CTCCTCTTG 60
 GCACTTCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCACCA ACTACCGCAA TGTCTCGGGC 120
 ATTTACCATG TCACCAATGA CTGCCCCGAAT TCAAGCATAG TGTTTGAGGC CGACCATCAC 180

91

ATCTTGCACC TTCCAGGATG CGTGCCCTGC GTGAAAGAGG GAAATCATTC ACGCTGCTGG 240
 GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG 300
 AGTCATGTGG ATGTGATGGT GGGGGCTGCC ACTGTTTGTG CAGCCCTTTA CATCGGGGAT 360
 CTGTGCGGTG GCTTGTTCTT GGTGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG 420
 ACTACCCAGG AATGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Gly Ile Asn Tyr Ala Thr Gly Xaa Leu Pro Gly Cys Ser Phe Ser
 1 5 10 15
 Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
 20 25 30
 Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 35 40 45
 Pro Asn Ser Ser Ile Val Phe Glu Ala Asp His His Ile Leu His Leu
 50 55 60
 Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn His Ser Arg Cys Trp
 65 70 75 80
 Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
 85 90 95
 Glu Ser Leu Arg Ser His Val Asp Val Met Val Gly Ala Ala Thr Val
 100 105 110
 Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
 115 120 125
 Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Glu
 130 135 140
 Cys Asn Cys Ser Ile
 145

92

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GACGGGATCA ATTATGCAAC AGGGAACCTC CCCGGTTGCT CTTTCTCTAT CTTTCATCCTG 60
GCACTTCTCT CGTGCCTGAC TGTCCCGGCC TCGGCTCAGC ATTATCGGAA TGTCTCGGGC 120
ATTTACCACG TCACCAACGA CTGCCC GAAC TCCAGCATAG TGTATGAGTC CGACCATCAC 180
ATCTTACACC TACCAGGGTG TGTACCCTGT GTGAAGACTG GGAACACTTC GCGCTGCTGG 240
GTGGCCTTAA CACCTACCGT GGCCGCGCCC ATACTTTCGG CTCCACTTAT GTCCGTACGG 300
CGGCATGTGG ATCTGATGGT GGGTGCAGCT ACCCTATCGT CTGCCCTCTA CGTTGGAGAC 360
CTCTGCGGGG GTGCCTTCCT AGTGGGGCAG ATGTTACCT TCCAGCCGCG TCGCCACTGG 420
ACTGTCCAAG ACTGCAACTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys

93

35 40 45
 Pro Asn Ser Ser Ile Val Tyr Glu Ser Asp His His Ile Leu His Leu
 50 55 60
 Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Thr Ser Arg Cys Trp
 65 70 75 80
 Val Ala Leu Thr Pro Thr Val Ala Ala Pro Ile Leu Ser Ala Pro Leu
 85 90 95
 Met Ser Val Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr Leu
 100 105 110
 Ser Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu Val
 115 120 125
 Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Val Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATGAGCACAC TTCAAACC CCAAAGAAAA ACCAAAAGAA ATACTAACCG TCGCCCTATG 60
 GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGTGGAG TTTACTTGTT GCCGCGCAGG 120
 GGCCCTCGTT TGGGTGTGCG CGCGACGAGA AAGACCTCCG AACGGTCCCA GCCTAGAGGC 180
 AGGCGCCAGC CCATACCAAA GGTACGCCAG CCGACAGGCC GTAGCTGGGG TCAACCCGGC 240
 TACCCTTGGC CCCTTTATGG CAACGAGGGC TCGGATGGG CGGGATGGCT CCTGTCCCCC 300
 CGCGGGTCTC GTCCTAATTG GGGCCCCAAC GACCCCCGGC GAAGGTCCCG CAACTTGGGT 360
 AAGGTCATCG ATACCCTTAC ATNCGGNCTA GCCGACCTCA TGGGGTACAT CCCTGTCCTA 420

94

GGAGGGCCGC TTGGCGGCGT TGCGGCTGCC CTGGCGCATG GCGTTAGGGC AATCGAGGAC 480
 GGGGTCAATT ACGCAACAGG GAATCTTCCT GGTGCTCCT TTTCTATCTT CCTCTTAGCA 540
 CTGTTATCGT GCCTCACTAC ACCAGCCTCA GCAATTCAAG TCAAGAACGC CTCTGGGATC 600
 TACCATCTTA CCAATGACTG CTCGAACAAC AGCATCGTTT TTGAGGCGGA GACCATGATA 660
 CTGCATCTTC CAGGTTGTGT CCCATGTATC AAGGCGGGGA ATGAGTCACG ATGTTGGCTC 720
 CCTGTCTCCC CCACCTTAGC CGTCCCCAAC TCATCAGTGC CAATCCACGG GTTTCGCCGA 780
 CACGTAGACC TCCTCGTTGG GGCAGCGGCA TTTTGTTCCG CCATGTACAT CGGAGACCTC 840
 TGTGGTAGCA TAATCTTGGT AGGGCAGCTT TTTACTTTCA GGCCTAAGTA CCATCAGGTT 900
 ACCCAGGATT GTAACGCTC TATNAACNCT GGCCACGTCA CGGGACACAG GATGGCA 957

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
		35					40					45			
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
		50				55					60				
Ile	Pro	Lys	Val	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly
65					70					75				80	
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
			85						90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
			100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Xaa

115 120 125
 Xaa Leu Ala Asp Leu Met Gly Tyr Ile Pro Val Leu Gly Gly Pro Leu
 130 135 140
 Gly Gly Val Ala Ala Ala Leu Ala His Gly Val Arg Ala Ile Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ile
 180 185 190
 Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu Thr Asn Asp Cys Ser
 195 200 205
 Asn Asn Ser Ile Val Phe Glu Ala Glu Thr Met Ile Leu His Leu Pro
 210 215 220
 Gly Cys Val Pro Cys Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu
 225 230 235 240
 Pro Val Ser Pro Thr Leu Ala Val Pro Asn Ser Ser Val Pro Ile His
 245 250 255
 Gly Phe Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys
 260 265 270
 Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Ser Ile Ile Leu Val Gly
 275 280 285
 Gln Leu Phe Thr Phe Arg Pro Lys Tyr His Gln Val Thr Gln Asp Cys
 290 295 300
 Asn Cys Ser Xaa Asn Xaa Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACCATCCG CCGCCCACAG 60
GACGTCAAGT TCCCGGGTGG CGGCCAGATC GTTGGTGGAG TCTACTTGCT GCCGCGCAGG 120
GGCCCGCGCT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCCAGAGGT 180
AGGCGCCAAC CAATACCCAA AGTGCGCCAC CAAACGGGCC GTACCTGGGC CCAGCCCGGG 240
TACCCCTGGC CTCTTTATGG AAATGAGGGC TGTGGTTGGG CAGGCTGGCT CCTGTCCCCC 300
CGCGGCTCTC GCCCAAATTG GGGCCCAAAC GACCCCGGC GGAGGTCCCG CAACTTGGGT 360
AAAGTCATCG ACACCCTTAC TTGCGGCTTC GCCGACCTCA TGGGGTATAT CCCTGTCGTA 420
GGCGCTCCGW TGGGAGGCGT CGCGNGGCC TTGGCGCATG GGGTCANGGN CATCGAGGAC 480
GGNGTAAATT ACGCAACAGN GAATCTTCCC GGNNGCTCTN TCTCTATCTT NCTCTTGGA 540
CTTCTCTCGT GCCTTACAAC ACCAGCCTCC GCGGCGCATT ATACCAACAA GTCTGGCCTG 600
TACCATCTCA CCAACGACTG CCCCAACAGC AGCATCGTTT ATGAGGCGGA GAACTGATT 660
TTGCACTTGC CTGGGTGTGT ACCTTGTGTG AAGRTGRACA ATCAATCCCG GTGCTGGGTG 720
CAGGCCTCCC CGACCCTGGC AGTGCCGAAC GCGTCTACGC CAGTCACCGG GTTCCGCAAA 780
CATGTGGACA TCATGGTGGG CGCTGCCGCG TTCTGTTTCTG CTATGTATGT GGGGGACCTG 840
TGCGGGGGCC TTTTCCTCGT TGGACAGCTC TTCACGCTCA GGCCTCGGAT GCATCAGGTT 900
GTCCAGGAGT GTAAGTGTTC CATCTACACA GGCATATCA CTGGACACCG AATGGCA 957

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Ile
1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala

97

35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Xaa
130 135 140

Gly Gly Val Ala Xaa Ala Leu Ala His Gly Val Xaa Xaa Ile Glu Asp
145 150 155 160

Xaa Val Asn Tyr Ala Thr Xaa Asn Leu Pro Xaa Xaa Ser Xaa Ser Ile
165 170 175

Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ala
180 185 190

His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu Pro
210 215 220

Gly Cys Val Pro Cys Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val
225 230 235 240

Gln Ala Ser Pro Thr Leu Ala Val Pro Asn Ala Ser Thr Pro Val Thr
245 250 255

Gly Phe Arg Lys His Val Asp Ile Met Val Gly Ala Ala Ala Phe Cys
260 265 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly
275 280 285

Gln Leu Phe Thr Leu Arg Pro Arg Met His Gln Val Val Gln Glu Cys
290 295 300

Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 45:

98

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATGAGCACAC TTCCTAAACC TCAAAGAAAA ACCAAACGAA ACACCAACCG TCGCCCACAG 60
 GACGTCAAGT TCCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACTTGTT GCCGCGCAGG 120
 GGCCCTCGTT TGGGTGTGCG CGCGACGAGG AAAACTTCTG AACGGTCCCA GCCCAGGGGT 180
 AGACGCCAAC CTATACCGAA GGTGCGTCAC CAAACGGGCC GTACCTGGGC TCAACCCGGG 240
 TACCCCTGGC CTCTTTATGG GAATGAGGGT TGTGGCTGGG CAGGGTGGCT CCTGTCCCCC 300
 CNCGGCTCTC GCCCTAATTG GGGCCCTAAT GACCCCCGN GGAGGTCCCG CAACCTGGGT 360
 AAGGTCATCG ATACCCTTAC TTGNGGSTTC GCCGACCTCA TAGAGTACAT TCC 413

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro

99

50 55 60

Ile Pro Lys Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Xaa Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110

Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa
115 120 125

Xaa Phe Ala Asp Leu Ile Glu Tyr Ile
130 135

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 957 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGAGCACAC TTCAAACCC CCAAAGAAAA ACCAAAAGAA ACACAAACCG TCGCCCAATG 60

GATGTCAAGT TCCCGGGCGG CGGTCAGATC GTTGGTGGAG TCTACTTGTT ACCGCGCAGG 120

GGCCCCACGTT TGGGTGTGCG CGCGACGAGG AAGACTTCGG AACGGTCCCA GGCCAGAGGT 180

AGGCGCCAAC CAATACCCAA GGTGCGCCAG AACCAAGGCC GAACCTGGGC TCAGCCTGGG 240

TACCCCTGGC CCCTTTATGG GAACGAGGGC TGCGGCTGGG CGGGGTGGCT CTTGTCCCCC 300

CGTGGCTCTC GCCCGGACTG GGGNCCCAAT GACCCCCGGN GGAGGTCCCG CAACCTGGGT 360

AAGGTCATCG ACACCCTCAC TTGCGGCTTC GCCGACCTCA TGGAGTACAT CCCTGTCGTT 420

GGCGCCCCC TTGGAGGCGT TCGGCGGAA CTGGNACATG GTGTCAGGGC CATCGAGGAC 480

GGGATAAACT ATGCAACAGG GAATCTTCCT GGTGCTCTT TCTCTATCTT CCWCTTGGCA 540

CTTCTCTCGT GCCTCACCAC GCCTGCCTCC GCACTAAACT ATGCTAACAA GTCTGGGCTG 600

TATCATCTAA CCAATGACTG CCCCAATAGC AGCATTGTGT ATGAGGCGAA TGGCATGATC 660
 CTGCATCTCC CGGGTTGCGT CCCCTGCGTG AAGACCGGCA ACCTGACCAA GTGTTGGCTG 720
 TCGGCCTCCC CGACATTGGC GGTGCAGAAT GCGTCGGTGT CCATCAGGGG TGTCCGCGAG 780
 CACGTGGACC TCTTGGTGGG TGCTGCTGCG TTCTGCTCTG CCATGTACGT GGGCGACTTA 840
 TCGGGTGGGC TCTTTCTCGT TGGGCAGTTG TTCACGTTCA GACCCAGGAT GTATGAGATC 900
 GCCCAGGACT GCAACTGTTC CATCTATGCA GGCCACATCA CTGGGCACCG GATGGCG 957

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Ala Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asp Trp Xaa Pro Asn Asp Pro
 100 105 110
 Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Glu Tyr Ile Pro Val Val Gly Ala Pro Leu
 130 135 140
 Gly Gly Val Ala Ala Glu Leu Xaa His Gly Val Arg Ala Ile Glu Asp

101

145 150 155 160
 Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Xaa Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Leu
 180 185 190
 Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro
 195 200 205
 Asn Ser Ser Ile Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu Pro
 210 215 220
 Gly Cys Val Pro Cys Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu
 225 230 235 240
 Ser Ala Ser Pro Thr Leu Ala Val Gln Asn Ala Ser Val Ser Ile Arg
 245 250 255
 Gly Val Arg Glu His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys
 260 265 270
 Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly
 275 280 285
 Gln Leu Phe Thr Phe Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp Cys
 290 295 300
 Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATGAGCACAC TTCCTAAACC ACAAAGAAAA ACCAAAAGAA ACACCAACCC CGGCCACAGG 60
 ACGTTAAGTT CCCAGGCGGC GGTCAGATCG TTGGTGGAGT TTACGTGCTA CCACGCAGGG 120

102

GCCCCAGTT GGGTGTGCGT GCAGTGCACA AGACTTCCGA GCGGTCGCAA CCTCGCAGTA 180
 GCGGCCAACC CATCCCCAGG GCGCGCCGAA CCGAGGGCAG GTCCTGGGCT CAGCCCGGGT 240
 ACCCTTGGCC CCTATATGGG AATGAGGGCT GCGGGTGGGC AGGGTGGCTC CTGTCCCCGC 300
 GCGGCTCTC 309

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Xaa Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Gln Leu Gly Val Arg Ala
 35 40 45
 Val Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Ser Arg Arg Gln Pro
 50 55 60
 Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg
 115

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

103

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GACGGAATTA ATTTGCAAC AGGGAATTTA CCTGGTTGCT CTTTCTCTAT CTTCTTCTG 60
GCTTTGTTCT CATGCTTGCT TACACCCACA GCCGGGCTGG AGTACCGTAA TGCCTCCGGA 120
CTCTACATGG TAACTAACGA CTGCAGTAAC GGTAGTATCG TGTATGAGGC CGGGGATATT 180
ATCCTCCACT TACCTGGCTG TGTCCCTGCG GTACGCTCTG GCAATACATC AAGATGCTGG 240
ATCCCTGTGA GCCCYACCGT CGCCGTGAAG TCGCCCTGCG CCGCCACCGC CTCTCTCCGC 300
ACGCACGTGG ATATGATGGT GGGRGCGGCC ACCCTATGCT CAGCTCTCTA CGTAGGAGAC 360
CTTTGTGGAG CGCTATTTCT TGTGCGGCAG GGGTTCTCAT GGAGACATCG CCAGCATTGG 420
ACTGTCCAGG ACTGCAACTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Leu Thr Pro Thr Ala Gly
20 25 30
Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val Thr Asn Asp Cys
35 40 45
Ser Asn Gly Ser Ile Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Ser Gly Asn Thr Ser Arg Cys Trp
65 70 75 80
Ile Pro Val Ser Xaa Thr Val Ala Val Lys Ser Pro Cys Ala Ala Thr

	85	90	95
Ala Ser Leu Arg Thr His Val Asp Met Met Val Xaa Ala Ala Thr Leu			
100	105	110	
Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ala Leu Phe Leu Xaa			
115	120	125	
Gly Gln Gly Phe Ser Trp Arg His Arg Gln His Trp Thr Val Gln Asp			
130	135	140	
Cys Asn Cys Ser Ile			
145			

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CTCGACAGTT ACTGAGAATG ACATCCGTGT CGAGGAATCA ATATACCAAT GTTGTGACTT	60
GGCCCCCGAG GCTCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACA TCGGGGGCCC	120
YCTAACCAAT TCAAAAGGAC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT	180
GACTACCAGC TGCGGCAACA CCCTGACATG CTACTTGAAA GCCAGAGCGG CCTGTGAGC	240
TGCAAAGCTC CGGGACTGCA CCATGCTCGT GTGCGGGGAT GACCTTGTCG TTATCTGTGA	300
GAGTGCGGGA GTCGAGGAAG ACGCGGCGAA CCTACGAGCT	340

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Ile Gly Gly Xaa Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80
Ala Lys Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CTCGACAGTT ACTGAGAACG ACATCCGTAC CGAGGRATCA ATCTATCAAT GTTGTGACTT 60
GGCCCCYGAG GCCCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACG TCGGGGGCCC 120
CCTAACCAAT TCAAAGGGGC AGAACTGCGG CTATCGTCGG TGTCGCGCTA GCGGCGTGCT 180
GACCACCAGC TGCGGCAACA CCCTCACATG CTAATTGAAA GCCAGGGCGG CCTGTGAGC 240
TGCAAAGCTC CAGGACTGCA CGATGCTCGT GTGCGGAGAC GACCTTGTCG TTATCTGTGA 300

106

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

c/ (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Thr	Glu	Xaa	Ser	Ile	Tyr	Gln
1				5					10					15	
Cys	Cys	Asp	Leu	Ala	Xaa	Glu	Ala	Arg	Lys	Ala	Ile	Lys	Ser	Leu	Thr
			20					25					30		
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	Gln	Asn
		35					40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Cys
	50					55					60				
Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Arg	Ala	Ala	Cys	Arg	Ala
65					70					75				80	
Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
			85						90					95	
Val	Ile	Cys	Glu	Ser	Ala	Gly	Val	Glu	Glu	Asp	Ala	Ala	Asn	Leu	Arg
			100					105					110		

Val

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CTCGACAGTT ACTGAGAACG ACATTCGTGT CGAGGAATCA ATCTACCAGT GCTGTGACTT 60
GGCCCCCGAG GCCCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTATA TCGGGGGTCC 120
CCTAACCAAC TCAAAGGGC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT 180
GACTACCAGC TGCGGTAATA CCCTCACATG TTACTTGAAA GCCAGGGCGG CCTGTGAGC 240
TGCGAAGCTC CAGGACTGCA CAATGCTCGT GTGCGGAGAC GACCTTGTCG TTATCTGTGA 300
GAGTGCRGGA GTCGAGGAGG ATGCGGCGAA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80
Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Xaa Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110
Val

(2) INFORMATION FOR SEQ ID NO: 59:

108

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 652 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG 60
TACACCGGAA TTGCCAGGAC GACCGGGTCC TTTCTTGGAT CAACCCGCTC AATGCCTGGA 120
GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGTG TTGGGTGCGG AAAGGCCTTG 180
TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCAGGAGG TCTCGTAGAC CGTGCACCAT 240
GAGCACGAAT CCTAAACCTC AAAGAAAAAC CAAAAGAAAC ACCAACCGCC GCCACAGGA 300
CGTCAAGTTC CCGGGCGGTG GCCAGATCGT TGGTGGAGTC TACGTGCTAC CGCGCAGGGG 360
CCCTAGATTG GGTGTGCGCG CAGCGCGGAA GACTTCGGAG CGGTCGCAAC CTCGTGGGAG 420
GCGCCAACCT ATTCCCAAGG AGCGCCGACC CGAGGGCAGG TCCTGGGCGC AGCCCCGGTA 480
CCCCTGGCCC CTCTATGGTA ACGAGGGCTG CGGGTGGGCA GGTNGGCTCC TGTCCCCTCG 540
CGGCTCCCGT CCTAGTTGGG GTCCTACTGA CCCCCGGCGT AGGTCACGCA ATTTGGGTAA 600
GGTCATCGAT ACCCTCACGT GTTGNTTCGC CGACCTCATG GGGTACATAC CG 652

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

109

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Xaa
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Xaa Phe Ala Asp Leu Met Gly Tyr Ile Pro
130 135

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTCAACGGTC ACTGAAGCTG ATATCCGAAC AGAGGAGTCC ATATACCAAT GCTGTGACCT 60

GCACCCCGAA GCACGTGTAG CCATCAAGTC TTTGACTGAA AGGCTGTACG TCGGGGGGCC 120

CTTGACCAAT TCAAAAGGGG AGAACTGCGG CTATCGCAGA TGCCGTGCCA GCGGCGTCTT 180

GACAACCAGC TGCGGCAACA CCCTCACCTG CTATATCAAG GCCCTAGCAG CCTGTAGAGC 240

TGCCAAGCTC CAGGACTGCA CCATGCTCGT CTGTGGCGAC GACCTGGTCG TGATCTGCGA 300

GAGTGTAGGG ACCCAGGAGG ATGCGGCGAG CCTGCGAGCC 340

110

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

21
Ser Thr Val Thr Glu Ala Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu His Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Glu Asn
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Arg Ala
65 70 75 80
Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Val Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO
///

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

NTCAACAGTC ACTGAGAGTG ATATCCGTAC AGAGGAGTCC ATCTACCAAT GCTGTGATCT 60
AGACCCCGAG GCTCGCAAGG CCATAAGGTC CCTCACAGAG AGGCTTTATA TCGGGGGTCC 120
CCTGACAAAC TCAAAAGGGC AGAACTGCGG CTACCGCCGA TGCCGTGCAA GCGGCGTCCT 180
GACGACTAGC TGCGGCAACA CCCTCACCTG TTACATAAAG GCCAGGGCAG CCTGTGCGAGC 240
TGCGAAGCTC CAGGATTGCT CAATGCTCGT CTGTGGCGAC GACCTTGTCG TTATCTGCGA 300
GATCGAGGGG NTCCANGAGG ATCCGTCGAN NNNNNNNNNN 340

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Ser Thr Val Thr Glu Ser Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu Asp Pro Glu Ala Arg Lys Ala Ile Arg Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80
Ala Lys Leu Gln Asp Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ile Glu Gly Xaa Xaa Glu Asp Pro Ser Xaa Xaa Xaa
100 105 110
Xaa

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

112

(A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CGTAGACCGT GCACCATGAG CACGAATCCT AAACCTCAAA GAAAAACCAA ACGTAACATC 60
AACCGCCGCC CACAGGACGT CAAGTTCCCG GCGGGTGGCC AGATCGTCGG TGGAGTTTAC 120
CTGTTGCCGC GCAGGGGCCC TAGATTGGGT GTGCGCGCGA CTAGGAAGAC TTCCGAGCGG 180
TCGCAACCTC GTGGGAGGCG ACAGCCTATC CCCAAGGCTC GCCGATCCGA GGGCAGGTCC 240
TGGGCTCAGC CCGGGTACCC TTGGCCCCCTC TATGGCAATG AGGGCATGGG TTGGGCAGGG 300
TGGCTCCTGT CCCCCCATGG CTCCCGGCCT AGTTGGGGCC CTTCAGACCC CCGGCGTAGG 360
TCGCGTAATT TGGGTAAGGT CATCGATACC CTCACATGCG GCTTCGCCGA CCTCATGGGG 420
TACATTCCGC TCGTCGGCGC CCCCCTAGGG GCGGTTGCCA GGGCCCTGGC GCAAGGCTTC 480
CGGGATCTAC CACGTCACCA ACGATTGTTC CAATGGGAGC ATTGTGTATG AGGCGGAAGG 540
CATGATCATG CATCTCCCCG GGTGCGTGCC CTGCGTTCGG GAAGGTAATA TCTCTCGTTG 600
CTGGGTACCG TTTTCCCCCA CGCTCGCAGC CAGGAATGCT AGCGTCCCCA CTCAGGCAAT 660
TCGGCGACAC GTCGACTTGC TTGTTGGGGC GGCCACACTC TGTTCTGCTA TGTATGTGGG 720
GGACCTCTGT GGGTCCGTCT TCCTCGTCGG CCAACTGTTC ACCTTCACAW CCCGCCAGNA 780
CTACACAGTG CAAGACTGCA ATTGTTCCAT CTACCCCGGC CATATAACGG G 831

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Ile Asn
1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
85 90 95
Leu Leu Ser Pro His Gly Ser Arg Pro Ser Trp Gly Pro Ser Asp Pro
100 105 110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
130 135 140
Gly Gly Val Ala Arg Ala Leu Ala Gln Gly Phe Arg Asp Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

NNNNNNNGTC ACTGAGAGTG ATATCCGTGT CGAGGARTCA ATTTACCAAT GCTGTGACCT 60
GGCCCCCGAG GCTCGCGTAG CCATAAAGTC GCTCACTGAG CGGCTATATG TCGGGGGCCC 120

114

TCTCACCAAC TCAAAGGAC AGAACTGCGG CTATCGCCGG TGCCGTGCGA GCGGTGTGCT 180
 GACTACTAGC TGCGGTAACA CCCTCACATG CTACCTGAAA GCCGCCGCGG CCTGTGCGAGC 240
 TGCAAAGCTC CGGGAATGCA CAATGCTCGT GTGTGGCGAC GACCTCGTCG TTATCTGTGA 300
 GAGTGCGGGG GTCCAGGAGG ATGCTGCAAG CCTNNNNNNN 340

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Xaa Xaa Val Thr Glu Ser Asp Ile Arg Val Glu Xaa Ser Ile Tyr Gln
 1 5 10 15
 Cys Cys Asp Leu Ala Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
 50 55 60
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ala Ala Cys Arg Ala
 65 70 75 80
 Ala Lys Leu Arg Glu Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Xaa Xaa
 100 105 110
 Xaa

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

115

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CTCGACAGTC ACAGAGAGAG ATATAAGNAC TGAGGAGTCC ATATACCAGG CTTGTTTCCTT 60
ACCCGAGCAG GCCAGAACTG CCATACACTC ATTGACTGAG AGACTCTACG TAGGAGGGCC 120
CATGATGAAC AGCAAAGGGC AATCCTGCGG ATACAGGCAT TGCCGCGCCA GCGGAGTGCT 180
CACCACCAGT ATGGGGAATA CCATCACGTG CTACATCAAG GCCCTAGCGG CTTGTAAAGC 240
AGCAGGAATA GTGGCCCCCA CCATGCTGGT GTGCGGCGAT GACCTAGTTG TCATCTCAGA 300
GAGTCAGGGA GTCGAGGAGG ACGACCGGAA CCTGANNNNN 340

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
35 40 45
Cys Gly Tyr Arg His Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50 55 60
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala
65 70 75 80
Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Gln Gly Val Glu Glu Asp Asp Arg Asn Leu Xaa
100 105 110

116

Xaa

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTCAACCGTC ACAGAGAGGG ATATAAGAAC TGAGGAGTCC ATATACCTGG CCTGCTCCTT 60
ACCCGAGCAG GCCCGGACTG CCATACATTC ATTAAGTGG AGACTTTACG TGGGAGGGCC 120
CATGATGAAC AGCAAAGGGC AGTCCTGCGG ATACAGGCGT TGCCGCGCTA GCGGAGTGCT 180
CACCACCAGT ATGGGGAACA CCATCACGTG TTATGTGAAA GCCCTCGCAG CTTGTAAAGC 240
TGCGGGCATT GTTGCCCCCA CGATGCTGGT GTGCGGCGAT GACCTGGTTG TCATCTCAGA 300
GAGTCAGGGG GCTGAGGAGG ACGAGCGAAA CCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1 5 10 15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser

117

35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
 50 55 60
 Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala
 65 70 75 80
 Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ser Glu Ser Gln Gly Ala Glu Glu Asp Glu Arg Asn Leu Arg
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CTCAACAGTC GCGGAGAGAG ACATCAGGAC CGAGGAGTCC ATTTACCTTG CCTGCTCCTT	60
ACCCGAGCAA GCCCGAACTG CCATACATTC ATTGACTGAG AGACTTTACG TAGGAGGGCC	120
CATGATGAAC AGCAAGGGAC AGTCCTGCGG TTACAGACGT TGCCGCGCCA GCGGAGTGCT	180
CACCACCAGC ATGGGGAATA CCATCACATG CTATGTGAAG GCATTAGCTG CCTGCAAAGC	240
TGCAGGCATC GTTGCTCCCA CGATGCTGGT TTGTGGCGAC GATCTGGTCA TCATCTCAGA	300
GAGTCAGGGA ACCGAGGAGG ATGAGCGGAA CCTGAGAGTC	340

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

118

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

cl

Ser	Thr	Val	Ala	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	Tyr	Leu	
1				5					10					15		
Ala	Cys	Ser	Leu	Pro	Glu	Gln	Ala	Arg	Thr	Ala	Ile	His	Ser	Leu	Thr	
			20					25					30			
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Met	Asn	Ser	Lys	Gly	Gln	Ser	
			35				40					45				
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Met	
	50					55					60					
Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Val	Lys	Ala	Leu	Ala	Ala	Cys	Lys	Ala	
65					70				75					80		
Ala	Gly	Ile	Val	Ala	Pro	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val	
				85				90						95		
Ile	Ile	Ser	Glu	Ser	Gln	Gly	Thr	Glu	Glu	Asp	Glu	Arg	Asn	Leu	Arg	
			100				105						110			
Val																

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGNACANCCT CCAGGCCCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG	60
TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGGAT AAACCCACTC TATGCCCCGGC	120
CATTTGGGCG TGCCCCGCA AGACTGCTAR CCGAGTAGCG TTGGGTTGCG AAAGGCCTTG	180

119

TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCAGGAGG TCTCGTAGAC CGTGCATCAT 240
 GAGCACAAAT CCTAAACCTC AAAGAAAAAC CAAAAGAAAC ACTAACCGCC GCCCACAGGA 300
 CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGAGTA TACTTGTTGC CNTGCAGGGG 360
 NCCCAGGTNG NGTNTATGCG CAACGANGAA GACTNCCGAA CAGTCCCAGC CACGTGGGAG 420
 GCGCCAGCCC ATCCCGAAAG ATCGGNGCAC CACTGGCAAG TCCTGGGGAC GTCCAGGATA 480
 TCCCTGGCCC CTGTATGGGA ACGAGGGCCT CGGGTGGGCA GGGTGGCTCC TGTCCCCCG 540
 GGGCTCCCGC CCGTCATGGG GCCCCACGGA CCCCCGGCAT AGGTCGCGCA ACTTGGGTAA 600
 GGTTCATCGAT ACCCTCACGT NCGGCTTTNC CGACCTCATG GGGTACATTC CCGTCGTTGG 660
 CGCCCCAGTA GGNNGGCGTCG CCAGAGCTCT CGCGCATGGC GTGAGAGTCC TGGAGGACGG 720
 GATAAACTAT GAAACAGGGA ACCTCCCCGG TTGCTCTTTC TCTATCTCCC TCCTTGCTCT 780
 TCTGTCCTGA ATTACCGNGC CAGTTTCTGC TGTGGAAATC AAAAACACCA GMAACACATA 840
 CATGGTGA CT AACGACTGTT CAAACAGYAG CATCACCTGG CAGCTTNGN NCGCGGTGCT 900
 TCACGTTCTT GGTGCGTCC CCTGTGAACG AGAGGGCAAC AGTTCCCGGT GCTGGATTCC 960
 AGTCACGCCC RACGTAKNCG TGAGCCGACC TGGTGCCCTA ACCGAGGGTT TGCGATCGCA 1020
 CATCGACACC ATCGTAGCGT CCGCAACATT TTGTTCTGCC CTCTACATAG GGGATGTATG 1080
 TGGCGCGATA ATGATAGCTG CCCAAGTGGT CATCGTCTCG CCGGAGCATC ATCACTTTGT 1140
 CCAGGACTGT AACTGTTCCA TCTACCCGGG CCACATAACG GGGCCTCGTA TGTNG 1195

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Xaa Cys Arg Xaa Pro Arg Xaa Xaa Xaa Cys Ala

120

35 40 45
 Thr Xaa Lys Thr Xaa Glu Gln Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Asp Arg Xaa Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa
 115 120 125
 Gly Phe Xaa Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
 130 135 140
 Xaa Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Ile Asn Tyr Glu Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Ser Leu Leu Ala Leu Leu Ser Ile Thr Xaa Pro Val Ser Ala Val Glu
 180 185 190
 Ile Lys Asn Thr Xaa Asn Thr Tyr Met Val Thr Asn Asp Cys Ser Asn
 195 200 205
 Xaa Ser Ile Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val Pro Gly
 210 215 220
 Cys Val Pro Cys Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro
 225 230 235 240
 Val Thr Pro Xaa Val Xaa Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
 245 250 255
 Leu Arg Ser His Ile Asp Thr Ile Val Ala Ser Ala Thr Phe Cys Ser
 260 265 270
 Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Ile Met Ile Ala Ala Gln
 275 280 285
 Val Val Ile Val Ser Pro Glu His His His Phe Val Gln Asp Cys Asn
 290 295 300
 Cys Ser Ile Tyr Pro Gly His Ile Thr Gly Pro Arg Met Xaa
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 77:

121

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATCCACAGTC ACTGAAAGAG ACATCAGAGT TGAAGAGTCC GTTTATCTGT CCTGTTCACT 60
TCCCGAGGAG GCCCGAGCTG CCATACACTC ACTAACTGAG AGGCTGTACG TGGGAGGTCC 120
CATGCAGAAC AGCAAGGGGC AATCCTGCGG ATACAGGCGC TGCCGCGCCA GCGGGGTGCT 180
CACCCTAGC ATGGGGAATA CTCTCACATG CTACTTGAAG GCCCAGGCGG CCTGCAGGGC 240
CGCGGGCATT GTTGCAACCA CAATGCTGGT GTGTGGCGAC GACCTGGTCG TCATCTCAGA 300
GAGTCAGGGG ACTGAGAGGG ACGAGAACAA CCTGAGACCT 340

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Ser Val Tyr Leu
1 5 10 15
Ser Cys Ser Leu Pro Glu Glu Ala Arg Ala Ala Ile His Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Gln Asn Ser Lys Gly Gln Ser
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50 55 60

122

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ser Glu Ser Gln Gly Thr Glu Arg Asp Glu Asn Asn Leu Arg
100 105 110

Pro

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CTCAACAGTC ACGGAGAGGG ACATCAGGAA TGAGGAGTCC ATATTCCTGG CCTGCTCGTT 60
 GCGGAGAGGAG GCGCGGACTG TCATACATTC GCTCACTGAG AGACTCTACA TAGGCGGGGCC 120
 GATGATGAAC AGCAAAGGCC AGTCCTGTGG ATACAGGCGT TGTCGCGCCA GCGGGGTGTT 180
 CACCACTAGC ATGGGCAATA CCATCACGTG CTATGTGAAA GCCATGGCAG CTTGCAGAGC 240
 TGCCGGGATT GACGCCCCCA CAATGTTGGT ATGTGGCGAC GACCTGGTGG TCATCTCAGA 300
 GAGTCAGGGG ACCGAGGAGG ACGAGCGAAA TCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

123

Ser Thr Val Thr Glu Arg Asp Ile Arg Asn Glu Glu Ser Ile Phe Leu
 1 5 10 15
 Ala Cys Ser Leu Pro Glu Glu Ala Arg Thr Val Ile His Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Ile Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
 50 55 60
 Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Met Ala Ala Cys Arg Ala
 65 70 75 80
 Ala Gly Ile Asp Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CTCTTGACTC TACTGTCACT GAACAGGATA TCAGGGTAGA AGAAGAAATA TACCAATGTT 60
 GTGACCTTGA GCCGGAGGCT AGACGGGCAA TCAAATCGCT CACGGAACGG CTTTACGTTG 120
 GAGGTCCCAT GTTCAACAGC AAGGGGCTCA AATGCGGATA TCGCCGTTGC CGTGCTAGCG 180
 GTGTATTGCC CACTAGCTAC GGTAATACAA TCACCTGCTA CATCAAGGCC AGAGCGGCTG 240
 CTCGAGCTGC GGGCCTTCAA GACCCATCAT TCCTTGCTCTG CGGAGATGAT TTGGTGGTAG 300
 TGGCTGAGAG TTGCGKCGTT GATGAGGAGG ATAGGGCAGC 340

124

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

1 Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
5 10 15
20 Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Lys Ser Leu Thr
25 30
35 Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Leu Lys
40 45
50 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Tyr
55 60
65 Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Arg Ala Ala Arg Ala
70 75 80
85 Ala Gly Leu Gln Asp Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
90 95
100 Val Val Ala Glu Ser Cys Xaa Val Asp Glu Glu Asp Arg Ala Ala Leu
105 110
Arg

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTCCACTGTA ACCGAAAAGG ACATCAGGCC CGAGGAAGAG GTCTATCAGT GTTGTGACCT 60
GGAGCCCGAA GCTCGCAAGG TTATTACCGC CCTCACAGAA AGACTCTACG TGGGCGGCCC 120
CATGCACAAC AGCAAGGGAG ACCTTTGTGG GTATCGGAGA TGCCGCGCAA GCGGCGTCTA 180
CACGACCAGC TTCGGAAACA CACTGACGTG CTACCTCAAA GCCTCAGCTG CTATTAGAGC 240
GGCAGGGCTG AGAGACTGCA CCATGCTGGT TTGCGGTGAC GACTTGGTCG TCATCGCTGA 300
GAGCGATGGC GTAGAGGAGG ATAACCGAGC CCTCCNAGCC 340

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ser Thr Val Thr Glu Lys Asp Ile Arg Pro Glu Glu Glu Val Tyr Gln
1 5 10 15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
65 70 75 80
Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Asn Arg Ala Leu Xaa
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:

126

(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CTCCACGGTG ACTGAAAAGG ACATCAGGGT CGAGGAAGAG ATCTATCAAT GTTGTGACCT 60
GGARCCCGAA GCCCGCAAAG CAATATCCGC CCTCACAGAG AGRCTCTACT TGGGCGGCCC 120
CATGTATAAC AGCAAAGGGG AGCTCTGCGG GTATCGGAGG TGCCGCGCGA GCGGAGTGTA 180
CACCACAAGT TTCGGGAACA CAGTGACCTG CTATCTTAAG GCCACCGCAG CTACCAGGGC 240
TGCAGGCCTA AAAGACTGCA CCATGCTGGT CTGCGGTGAC GACTTGGTCG TCATCGCCGA 300
GAGCGAGGGC GTAGAGGAGG ATTCCCAACC CCTCCGAGCC 340

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu Xaa Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr
20 25 30
Glu Xaa Leu Tyr Leu Gly Gly Pro Met Tyr Asn Ser Lys Gly Glu Leu
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50 55 60
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
65 70 75 80

127

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Glu Gly Val Glu Glu Asp Ser Gln Pro Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTCCACCGTA ACCGAAAGGG ACATCAGGGT CGAGGAGGAG GTCTATCAGT GTTGTGATCT 60
GGAGCCAGAG GCCCGCAAGG CAATATCCGC CCTCACGGAG AGACTCTATG TGGGCGGTCC 120
CATGTTTAAC AGCAAGGGAG ACCTATGTGG CTACCGCAGG TGCCGCGCAA GCGGCGTCTA 180
CACCACCAGC TTCGGAAACA CACTGACCTG CTACCTCAAG GCCACGGCCG CTACCAGAGC 240
GGCCGGCCTG AAGGATTGCA CAATGCTGGT TTGCGGGGAC GACCTGGTCG TCATCGCAGA 300
GAGCGATGGC GTGGACGAGG ACCGCCGAGC CCTCCAAGCT 340

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln

128

1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Arg Ala Leu Gln
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

CTCAACAGTC ACAGAGCGCG ATGTCCAGAC GGAGCATGAC ATCTACCAGT GCTGTAAGTT 60

GGAGCCCGCA GCACGGACAG CCATCACATC GCTTACTGAC CGATTGTACT NCGGTGGTCC 120

CATGTNTAAC TCTAAAGGTC AGGCATGTGG ATACCGTAGG TGCAGGGCCA GTGGCGTCTT 180

GACCACCATC CTGGCCAATA CTCTGACTTG CTACTTGAAA GCTCAGGCGG CATGCAGAGC 240

TGCCGGGCTG AAGGACTTTG ACATGTTGGT CTGCGGAGAC GACCTTGTCG TTATTTCCGA 300

GAGTTTGGGG GTCTCGGAGG AACTAGTGC ACTGCGAGCT 340

(2) INFORMATION FOR SEQ ID NO: 90:

129

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

21

Ser Thr Val Thr Glu Arg Asp Val Gln Thr Glu His Asp Ile Tyr Gln
1 5 10 15

Cys Cys Lys Leu Glu Pro Ala Ala Arg Thr Ala Ile Thr Ser Leu Thr
 20 25 30

Asp Arg Leu Tyr Xaa Gly Gly Pro Met Xaa Asn Ser Lys Gly Gln Ala
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ile Leu
50 55 60

Ala Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80

Ala Gly Leu Lys Asp Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Ser Glu Ser Leu Gly Val Ser Glu Asp Thr Ser Ala Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

130

CTCGACAGTC ACCGAGCGCG ACATCCRCAC CGAGCACGAC ATCTACCAAT GCTGCCAACT 60
 TGACCCGGTG GCACGCAAGG CTATTACATC TCTGACTGAG CGGCTGTACT GCGGWGGGCC 120
 CATGATGAAC TCCCGTGGTC AATCATGTGG ATACCGTAGG TGCCGAGCCA GTGGCGTGCT 180
 CACCACGAGC TTGGGCAATA CCCTAACATG CTATTTGAAA GCACAAGCAG CGTGTAGGGC 240
 AGCAAAGCTC AAAAAGTATG ACATGTTAGT CTGCGGAGAC GATCTAGTCG TTATCGCGGA 300
 GAGTGGAGGA GTCTCTGAGG ATGTTGACGC CCTGCGAGCA 340

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu His Asp Ile Tyr Gln
 1 5 10 15
 Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Cys Xaa Gly Pro Met Met Asn Ser Arg Gly Gln Ser
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Leu
 50 55 60
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
 65 70 75 80
 Ala Lys Leu Lys Asn Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ala Glu Ser Gly Gly Val Ser Glu Asp Val Asp Ala Leu Arg
 100 105 110
 Ala

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid

131

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTCCTCCGTC ACGGAGCGTG ACATCCGCAC TGAACACGAC ATCTATCAGT GCTGCCAATT 60
AGATCCGGTA GCACGGAAAG CCATTACATC TCTTACTGAG CGGCTGTACT GCGGCGGCCC 120
CATGTACAAC TCTCGAGGTC AGTCATGTGG GTACCGCAGG TGCCGGGCTA GTGGTGTCTT 180
CACCACAAGC TTGGGCAACA CCATGACATG CTACCTGAAG GCTCAGGCGG CTTGTAGGGC 240
AGCRAAGCTC AAAAAGTTTG ACATGTTGGT CTGCGGAGAC GACCTAGTCG TTATTGCTGA 300
GAGCGGAGGA GTCCCTGAGG ATGCCGGGGC CCTGCGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Ser Ser Val Thr Glu Arg Asp Ile Arg Thr Glu His Asp Ile Tyr Gln
1 5 10 15
Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Arg Gly Gln Ser
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60
Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80
Xaa Lys Leu Lys Asn Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val

132

85

90

95

Val Ile Ala Glu Ser Gly Gly Val Pro Glu Asp Ala Gly Ala Leu Arg
 100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ATCCACAGTC ACGGGGCGCG ACATACGCAC AGAACNAGAC ATTTACCTGT CCTGCCAGCT 60
 CGACCCAGAG GCCCGGAAAG CCATAAAGTC TCTCACTGAG AGGCTCTATG TCGGGGGCCC 120
 TATGTACAAC TCAAAGGGCC AACTCTGTGG TCAACGCCGA TGCCGAGCAA GCGGAGTACT 180
 CCCCACAAGC ATGGGTAACA CCATCACATG CTTCTGAAG GCAACCGCCG CTTGCCGAGC 240
 AGCCGGCTTT ACAGATTATG ACATGTTGGT CTGCGGAGAC GATTTGGTTG TCGTAACTGA 300
 GAGTGCTGGA GTCAACGAGG ATATCGCTAA CCTGCGAGCC 340

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Ser Thr Val Thr Gly Arg Asp Ile Arg Thr Glu Xaa Asp Ile Tyr Leu
 1 5 10 15

133

Ser Cys Gln Leu Asp Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Leu
 35 40 45
 Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Met
 50 55 60
 Gly Asn Thr Ile Thr Cys Phe Leu Lys Ala Thr Ala Ala Cys Arg Ala
 65 70 75 80
 Ala Gly Phe Thr Asp Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Val Thr Glu Ser Ala Gly Val Asn Glu Asp Ile Ala Asn Leu Arg
 100 105 110
 Ala

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CTCCACTGTC ACTGAGCAGG ACATCAGGGT AGAACTTTCC ATCTTTCAGG CCTGTGACCT	60
CAAGGACGAG GCTAGGAGGG TGATAACTTC ACTCACGGAG CGGCTTTACT GTGGTGGTCC	120
TATGTTCAAC AGCAAGGGAC AACACTGCGG TTACCGCCGC TGCCGTGCTA GTGGGGTGCT	180
ACCCACCAGC TTCGGGAACA CAATCACCTG TTACATCAAA GCAAAGGCAG CTACCAAAGC	240
TGCCGGAATT AAAAATCCAT CATTCCTTGT CTGCGGAGAT GACTTGGTCG TGATTGCTGA	300
GAGTGCAGGG ATCGATGAGG ACAAGAGCGC CTTGAGAGCT	340

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:

134

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

1 Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Leu Ser Ile Phe Gln
5 10 15
20 Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
25 30
35 Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
40 45
50 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
55 60
65 Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
70 75 80
85 Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
90 95
100 Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Lys Ser Ala Leu Arg
105 110
Ala

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTCTACCGTC ACAGAGAGGG ACATACGGAC AGAAGAATCC ATCTATCTGT CTTGTCAATT

60

135

GCCTGAAGAG GCCCGGAAAG CCATTAAATC GCTGACAGAG AGACTATACG TGGGCGGCCC 120
 GATGGAAAAC AGCAAGGGCC AGGCTTGCGG ATATAGGCGT TGCCGCGCAA GCGGGGTATT 180
 CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAA GCTAAAGCGG CTTGTAAAGC 240
 CGCTGGCATT GTAGACCCGG TGATGCTCGT GTGCGGTGAC GACCTAGTGG TCATCTCAGA 300
 AAGCAAGGGG GTGGAGGAGG ACCAGCGGGA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
 1 5 10 15
 Ser Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
 50 55 60
 Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala
 65 70 75 80
 Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

136

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTCCACTGTC ACTGAGAGAG ACATACGGAC AGAAGAATCC ATCTAYYTGG CTTGTCAATT 60
GCCCCGAAGAG GCCCGGAAGG CATTAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC 120
GATGGAAAAC AGCAAAGGCC AGGCCTGCGG ATATAGGCGT TGCCGCGCAA GCGGGGTATT 180
CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAG GCCAARGCAG CTTGTAAAGC 240
YGCTGGCATT GTTGACCCGG TGATGCTCGT GTGCGGCGAC GACCTAGTGG TCATCTCAGA 300
GAGCAAGGGG GTAGAGGAGG ACCAGCGAGA CCTAC 335

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Xaa Xaa
1 5 10 15
Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Xaa Ala Ala Cys Lys Xaa
65 70 75 80
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

137

Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Xaa
 100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG 60
 TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGGAT TAACCCACTC TATGCCCCGA 120
 GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGCG TTGGGTTGCG AAAGGCCTTG 180
 TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCAGGAGG TCTCGTAGAC CGTGCAACCAT 240
 GAGCACGAAT CCTAAACCTC AAAGACAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA 300
 CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGGGTG TACTTGTTGC CGCGCAGGGG 360
 CCCCAGAGTG GGTGTGCGCG CGACGAGAAA GACCTCGGAG CGGTCCCAGC CGCGTGGGAG 420
 GCGCCAACCT ATCCCCAAGG TTAGGCGCAC CACCGGCCGT T 461

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Met Ser Thr Asn Pro Lys Pro Gln Arg Gln Thr Lys Arg Asn Thr Asn

138

c1

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

CTCTACTGTC	ACAGAGAGGG	ATATACGAAC	AGAGGAATCC	ATYTATCTGG	CTTGTC AATT	60
GCCCGAAGAG	GCCCGGAAGG	CCATCAAATC	ACTGACAGAG	AGACTATACG	TGGGCGGCCC	120
GATGGAAAAC	AGCAAGGGCC	AGGCCTGCGG	ATACAGGCGT	TGCCGCGCAA	GCGGGGTATT	180
CACCACAAGC	TTGGGGAACA	CCATGACTTG	TTACATCAA	GCCAAGGCGG	CTTGTAAGC	240
CGCTGGCATT	GTTGACCCAG	TGATGCTCGT	GTGCGGCGAC	GACCTAGTGG	TCATCTCAGA	300
AAGCAAGGGG	GTGGAGGAGG	ACCAACGAGA	CCTACGANTC			340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

cl

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Xaa	Tyr	Leu
1				5				10						15	
Ala	Cys	Gln	Leu	Pro	Glu	Glu	Ala	Arg	Lys	Ala	Ile	Lys	Ser	Leu	Thr
		20						25					30		
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Glu	Asn	Ser	Lys	Gly	Gln	Ala
		35					40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	Leu
	50					55					60				
Gly	Asn	Thr	Met	Thr	Cys	Tyr	Ile	Lys	Ala	Lys	Ala	Ala	Cys	Lys	Ala
65					70				75					80	
Ala	Gly	Ile	Val	Asp	Pro	Val	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
			85					90						95	
Val	Ile	Ser	Glu	Ser	Lys	Gly	Val	Glu	Glu	Asp	Gln	Arg	Asp	Leu	Arg
			100					105						110	
															Xaa

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ala	Arg	Gln	Ser	Asp	Gly	Arg	Ser	Trp	Ala	Gln
1			5					10		

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Asp Arg Arg Thr Thr Gly Lys Ser Trp Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 112:

141

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Asp Arg Arg Ala Thr Gly Arg Ser Trp Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Asp Arg Arg Ala Thr Gly Lys Ser Trp Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Val Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

142

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

143

Val Arg Arg Thr Thr Gly Arg Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Val Arg Arg Thr Thr Gly Arg Thr Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:

144

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Tyr Glu Val His Ser Thr Thr Asp Gly Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Val Glu Val Lys Asn Thr Ser Gln Ala Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Ile Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Gln Val Lys Asn Thr Ser His Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Val Glu Ile Lys Asn Thr Xaa Asn Thr Tyr Val Leu
1 5 10

146

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Glu Ile Lys Asn Thr Ser Asn Thr Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid

147

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ile Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

C1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Leu Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 139:

149

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

ISO

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Val Trp Gln Leu Xaa Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Val Trp Gln Leu Arg Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Ile Trp Gln Met Gln Gly Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

151

Val Trp Gln Leu Lys Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Val Trp Gln Leu Glu Glu Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Val Tyr Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:

BSZ

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Val Tyr Glu Ala Asp His His Ile Leu Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Val Phe Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Val Tyr Glu Ser Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Val Phe Glu Glu Thr Met Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu
1 5 10

194

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Val Arg Glu Asp Asn His Leu Arg Cys Trp Met Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Met Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val Leu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Glu Asn Ser Ser Gly Arg Phe His Cys Trp Ile Pro Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Glu Arg His Gln Asn Gln Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

C1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Val Arg Glu Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 166:

157

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Val Arg Val Gly Asn Gln Ser Ser Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

158

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Val Lys Glu Gly Asn His Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Val Lys Thr Gly Asn Thr Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

159

Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val Gln Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu Ser Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Val Arg Ser Gly Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Val Lys Asn Ala Ser Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:

160

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Val Lys Asp Ala Asn Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Ala Arg Ile Ala Asn Ala Pro Ile Asp Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Val Ser Lys Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Val Ser Arg Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Val Asn Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Val Ser Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

162

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Ala Pro Tyr Thr Ala Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid

163

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Ala Pro Ile Leu Ser Ala Pro Leu Met Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Val Pro Asn Ser Ser Val Pro Ile His Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Val Pro Asn Ala Ser Thr Pro Val Thr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Val Gln Asn Ala Ser Val Ser Ile Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Val Lys Ser Pro Cys Ala Ala Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Ser Pro Arg Met His His Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Ser Pro Arg Leu Tyr His Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 193:

165

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Thr	Ser	Arg	Arg	His	Trp	Thr	Val	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Ala	Pro	Lys	Arg	His	Tyr	Phe	Val	Gln	Glu
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser	Pro	Gln	Tyr	His	Thr	Phe	Val	Gln	Glu
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

166

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Ser	Pro	Gln	His	His	Asn	Phe	Ser	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Ser	Pro	Gln	His	His	Ile	Phe	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Ser	Pro	Glu	His	His	His	Phe	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

167

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Arg Pro Arg Arg His Trp Thr Ala Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Arg Pro Arg Arg His Trp Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:

168

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Gln	Pro	Arg	Arg	His	Trp	Thr	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Arg	Pro	Lys	Tyr	His	Gln	Val	Thr	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Arg	Pro	Arg	Met	His	Gln	Val	Val	Gln	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 207:

C1 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Arg His Arg Gln His Trp Thr Val Gln Asp
1 5 10

170